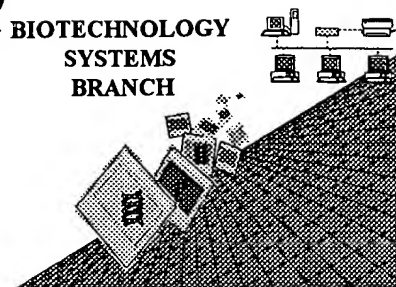


RAW SEQUENCE LISTING **ERROR REPORT**

BIOTECHNOLOGY
SYSTEMS
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number: 09/305,984

Art Unit / Team No. : 0186

Date Processed by STIC: 5/18/99

THE ATTACHED PRINTOUT EXPLAINS THE ERRORS DETECTED.

PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,

2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY

THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.

IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:

ARTI SHAH 703-308-4212

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/305,984

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 ☐ Wrapped Aminos The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 ☐ Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 ☐ Misaligned Amino Acid Numbering The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 ☐ Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 ☐ Variable Length Sequence(s) ____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7 ☐ PatentIn ver. 2:0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence.
- 8 ☐ Skipped Sequences (OLD RULES) Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 ☐ Skipped Sequences (NEW RULES) Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 10 ☐ Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 ☐ Use of <213>Organism (NEW RULES) Sequence(s) ____ are missing this mandatory field or its response.
- 12 ☐ Use of <220>Feature (NEW RULES) Sequence(s) ____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 ☒ PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/305,984

DATE: 05/18/1999
TIME: 08:42:27

Input Set: I305984.RAW

This Raw Listing contains the General Information
Section and up to first 5 pages.

*see item 13 on Enr summary sheet for
Hydronation of these missing
mandatory items*

see item 13

*Does Not Comply
Corrected Diskette Needed*

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E--> 2 <120>
W--> 3 <130>
      4 <140> US/09/305,984
      5 <141> 1999-05-05
E--> 6 <160>
      7 <170> PatentIn Ver. 2.0
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     16 <211> 25
     17 <212> PRT
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     22         Asp Lys Arg Pro Ala Arg Asp Tyr Asn
     23             20             25
     24 <210> 3
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     27 <213> Artificial Sequence
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     36 <213> Artificial Sequence
     37 <220>
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     41             1             5             10             15
     42         Asp Lys Arg Pro Ala Arg Asp Tyr Asn
     43             20             25
     44 <210> 5
  
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RAW SEQUENCE LISTING
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48 <220>
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55 <212> PRT
56 <213> Artificial Sequence
57 <220>
58 <223> Description of Artificial Sequence:primer
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67 <213> bacterial
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71 <211> 14
72 <212> PRT
73 <213> bacterial
74 <400> 8
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77 <210> 9
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79 <212> DNA
80 <213> bacterial
81 <400> 9
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83 <210> 10
84 <211> 11
85 <212> PRT
86 <213> bacterial
87 <400> 10
88   Leu Ala Asp Lys Arg Pro Ala Arg Asp Tyr Asn
89       1           5           10
90 <210> 11
91 <211> 84
92 <212> DNA
93 <213> bacterial
94 <400> 11

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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/305,984

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96      aaaaggccag caagagacta taat                                     84
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101     <400> 12
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104     Leu Leu Ala Asp Lys Arg Pro Ala Arg Asp Tyr Asn
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113     cgtcaggaaa ccattgggtca aaaggcaaca gccattgccc agtccctaga agggaaagat 180
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115     gtcaaagggtg agatgaccga ggacaagtta gaagtcaagg acagtcttcc tctggacaca 300
116     gaccgccaga caacctctct ctttattgag gagcgcgagg tgaaaacgca agacggtggt 360
117     actatgattc tccagtttct agcttccatg gatttacaaa aggaagcggg gcaaatcagt 420
118     ctccagtttc ttccctatac cttgctggcc tcctttctga tttccctttt ggtggcctac 480
119     atctacgctc ggactattgt tgcaccgatt ttggaaatca agcgggtgac ccgtcggatg 540
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121     aaggaacaaa tcaatagcct ctaccagcat ctcttgactg ttattgcgga cttgcatgaa 660
122     aagaatgaag ccattctcca gctggagaag atgaaggctg aattcctacg aggagcttct 720
123     catgaattga aaacaccgct ggctagtttg aaaatcctaa tcgaaaatat gagagagaat 780
124     atcggtcggt ataaggatag agaccagtat ctgggagttg ccttggggat tgtggatgaa 840
125     ctcaatcacc atgttctgca gatactttcc ctctctctg tgcaggaatt gcgagatgat 900
126     agggaaacaa ttgacctcct ccagatgacg caaaatctgg tcaaagatta tgccttgcta 960
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129     ccaggtggct tagttcgaat tggagaaaga gaaggagaac tttttatcga aaatagctgt 1140
130     agtcagaggg aacaagaaaa actagcccag tctttttctg acaatgccag tcgcaagggtc 1200
131     aaggggtctg gtatggggct ctttggtggtt aagagtctat tagaacatga aaaattagct 1260
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137     <213> bacterial
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141     Ile Phe Ser Val Leu Val Ile Cys Leu His Leu Ala Ile Tyr Phe Leu
142           20             25             30
143     Phe Pro Ser Thr Tyr Leu Ser His Arg Gln Glu Thr Ile Gly Gln Lys
144           35             40             45

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145   Ala Thr Ala Ile Ala Gln Ser Leu Glu Gly Lys Asp Arg Gln Ser Ile
146       50                               55                               60
147   Glu Gln Val Leu Asp Leu Tyr Ser Gln Thr Ser Asp Ile Lys Gly Thr
148       65                               70                               75                               80
149   Val Lys Gly Glu Met Thr Glu Asp Lys Leu Glu Val Lys Asp Ser Leu
150                               85                               90                               95
151   Pro Leu Asp Thr Asp Arg Gln Thr Thr Ser Leu Phe Ile Glu Glu Arg
152                               100                               105                               110
153   Glu Val Lys Thr Gln Asp Gly Gly Thr Met Ile Leu Gln Phe Leu Ala
154                               115                               120                               125
155   Ser Met Asp Leu Gln Lys Glu Ala Glu Gln Ile Ser Leu Gln Phe Leu
156       130                               135                               140
157   Pro Tyr Thr Leu Leu Ala Ser Phe Leu Ile Ser Leu Leu Val Ala Tyr
158   145                               150                               155                               160
159   Ile Tyr Ala Arg Thr Ile Val Ala Pro Ile Leu Glu Ile Lys Arg Val
160                               165                               170                               175
161   Thr Arg Arg Met Met Asp Leu Asp Ser Gln Val Arg Leu Arg Val Asp
162                               180                               185                               190
163   Ser Lys Asp Glu Ile Gly Asn Leu Lys Glu Gln Ile Asn Ser Leu Tyr
164       195                               200                               205
165   Gln His Leu Leu Thr Val Ile Ala Asp Leu His Glu Lys Asn Glu Ala
166       210                               215                               220
167   Ile Leu Gln Leu Glu Lys Met Lys Val Glu Phe Leu Arg Gly Ala Ser
168   225                               230                               235                               240
169   His Glu Leu Lys Thr Pro Leu Ala Ser Leu Lys Ile Leu Ile Glu Asn
170                               245                               250                               255
171   Met Arg Glu Asn Ile Gly Arg Tyr Lys Asp Arg Asp Gln Tyr Leu Gly
172                               260                               265                               270
173   Val Ala Leu Gly Ile Val Asp Glu Leu Asn His His Val Leu Gln Ile
174       275                               280                               285
175   Leu Ser Leu Ser Ser Val Gln Glu Leu Arg Asp Asp Arg Glu Thr Ile
176       290                               295                               300
177   Asp Leu Leu Gln Met Thr Gln Asn Leu Val Lys Asp Tyr Ala Leu Leu
178   305                               310                               315                               320
179   Ala Lys Glu Arg Glu Leu Gln Ile Asp Asn Ser Leu Thr His Gln Gln
180                               325                               330                               335
181   Ala Tyr Leu Asn Pro Ser Val Met Lys Leu Ile Leu Ser Asn Leu Ile
182       340                               345                               350
183   Ser Asn Ala Ile Lys His Ser Val Pro Gly Gly Leu Val Arg Ile Gly
184       355                               360                               365
185   Glu Arg Glu Gly Glu Leu Phe Ile Glu Asn Ser Cys Ser Ser Glu Glu
186       370                               375                               380
187   Gln Glu Lys Leu Ala Gln Ser Phe Ser Asp Asn Ala Ser Arg Lys Val
188   385                               390                               395                               400
189   Lys Gly Ser Gly Met Gly Leu Phe Val Val Lys Ser Leu Leu Glu His
190                               405                               410                               415
191   Glu Lys Leu Ala Tyr Arg Phe Glu Met Glu Glu Asn Ser Leu Thr Phe
192       420                               425                               430
193   Phe Ile Asp Phe Pro Lys Val Val Gln Asp
194       435                               440

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RAW SEQUENCE LISTING
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202 tctagctatg aggtggccct ggttttactg gatatccaga tgcccaagct caacggctta 180
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206 acaggacgaa tcttttctta caaggatacc aagggtggact ttgaaagcta cagtgcagc 420
207 ctgcgaggtc aagaagtgcc tatcaatgcc aaagagttgg aaattctgga ctatctagt 480
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209 gatgagggtt cctttgaccg tgttattgat gtttatatca aggaattgcg gaaaaagcta 600
210 gacttggatt gtatcctcac tgtgcgcaat gttggttata aattggagcg aaaatga 657

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY
PATENT APPLICATION US/09/305,984DATE: 05/18/1999
TIME: 08:42:27

Input Set: I305984.RAW

Line	? Error/Warning	Original Text
1	E Response to "Applicant" Name is Missing	
2	E Response to "Title of Invention" Missing	
3	W Response to "File Reference" is Missing	
6	E # of Seq. 0 Not Equal Actual 54	
809	W "N" or "Xaa" used: Feature required	Asp Lys Arg Pro Ala Arg Asp Xaa Asn
834	W "N" or "Xaa" used: Feature required	Arg Lys Glu Phe His Xaa Xaa Xaa Xaa Xaa X
836	W "N" or "Xaa" used: Feature required	Lys Arg Pro Xaa Arg Asp Tyr
872	W "N" or "Xaa" used: Feature required	Met Xaa Xaa Xaa Xaa Xaa Asn Val Leu Ser X
874	W "N" or "Xaa" used: Feature required	Xaa Xaa Xaa Xaa Ala Xaa Xaa Xaa Asn